

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 00:48:43 ; search time 2351.15 seconds
(without alignments)

168.399 Million cell updates/sec

Title: US-09-851-670-16

Sequence: 24
1 gtccaagcagcagcaatttcgca 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hlg: *
3: gb_in: *
4: gb_ov: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
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12: gb_sy: *
13: gb_un: *
14: gb_vi: *
15: em_ba: *
16: em_fun: *
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25: em_ro: *
26: em_sts: *
27: em_sy: *
28: em_un: *
29: em_vi: *
30: em_higo_hum: *
31: em_higo_inv: *
32: em_higo_rod: *
33: em_hlg_hum: *
34: em_hlg_inv: *
35: em_hlg_rod: *
36: em_hlg_other: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

8

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	14.6	60.8	27	6	AX049980	AX049980 Sequence
C 2	14.2	59.2	30	6	I49785	I49785 Sequence 8
C 3	14.2	59.2	44	6	A98898	A98898 Sequence 6
4	14	58.3	28	6	AR090191	AR090191 Sequence
5	14	58.3	51	6	AX158351	AX158351 Sequence
6	13.6	56.7	26	6	AR008926	AR008926 Sequence
7	13.6	56.7	26	6	AR087621	AR087621 Sequence
C 8	13.6	56.7	48	6	A06322	A06322 Artificial
C 9	13.6	56.7	48	6	A06323	A06323 Artificial
C 10	13.6	56.7	48	6	AX033196	AX033196 Sequence
C 11	13.4	55.8	41	6	A59035	A59035 Sequence 23
C 12	13.4	55.8	45	6	A59036	A59036 Sequence 24
C 13	13.2	55.0	19	6	AX130478	AX130478 Sequence
C 14	13.2	55.0	21	6	AX145829	AX145829 Sequence
C 15	13.2	55.0	23	6	AX111191	AX111191 Sequence
C 16	13.2	55.0	39	6	AR067715	AR067715 Sequence
C 17	13.2	55.0	39	6	AR079910	AR079910 Sequence
C 18	13.2	55.0	39	6	AR083849	AR083849 Sequence
C 19	13.2	55.0	39	6	I13243	I13243 Sequence 3
C 20	13.2	55.0	39	6	I21420	I21420 Sequence 3
C 21	13.2	55.0	39	6	I30304	I30304 Sequence 3
C 22	13.2	55.0	45	6	A67371	A67371 Sequence 12
C 23	13.2	55.0	47	6	AX114361	AX114361 Sequence
C 24	13.2	55.0	51	6	AX159777	AX159777 Sequence
C 25	13.2	55.0	51	6	AX159778	AX159778 Sequence
C 26	13.2	55.0	51	6	AX160740	AX160740 Sequence
27	13	54.2	23	6	AR090696	AR090696 Sequence
28	13	54.2	31	6	AX155961	AX155961 Sequence
29	13	54.2	31	6	AX155973	AX155973 Sequence
30	13	54.2	46	6	A20984	A20984 Oligonucleo
C 31	13	54.2	48	6	AR032596	AR032596 Sequence
C 32	13	54.2	48	6	I29336	I29336 Sequence 20
C 33	13	54.2	48	6	I91010	I91010 Sequence 20
C 34	13	54.2	51	6	AX159391	AX159391 Sequence
C 35	13	54.2	51	6	AX160312	AX160312 Sequence
36	12.8	53.3	19	6	AR016648	AR016648 Sequence
37	12.8	53.3	19	6	AR110271	AR110271 Sequence
38	12.8	53.3	20	6	I27757	I27757 Sequence 3
39	12.8	53.3	24	6	AR153416	AR153416 Sequence
C 40	12.8	53.3	29	6	AR145508	AR145508 Sequence
C 41	12.8	53.3	31	6	AR088617	AR088617 Sequence
C 42	12.8	53.3	35	11	C75921	C75921 Homo sapien
C 43	12.8	53.3	37	6	AR122688	AR122688 Sequence
C 44	12.8	53.3	42	6	AR079489	AR079489 Sequence
45	12.8	53.3	50	6	AX157240	AX157240 Sequence

ALIGNMENTS

RESULT 1
LOCUS AX049980/c
DEFINITION Sequence 81 from Patent WO0070071.
ACCESSION AX049980
VERSION AX049980.1 GI:12226357
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE
1 (bases 1 to 27)
Bout,A., Havenaga,M.J. and Vogels,R.
Adenovirus derived gene delivery vehicles comprising at least one
element of adenovirus type 35
Patent: WO 0070071-A 81 23-NOV-2000;
JOURNAL
Introgene B.V. (NL)
FEATURES
source
1..27
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"

AR008926
LOCUS AR008926 26 bp DNA
DEFINITION Sequence 51 from patent US 5756083.
ACCESSION AR008926
VERSION AR008926.1 GI:3967731
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 26)
TITLE Elliot,S.G.
JOURNAL Mpl ligand analogs
FEATURES Patent: US 5756083-A 51 26-MAY-1998;
Location/Qualifiers
source 1..26
BASE COUNT 8 a 7 c 8 g 3 t
ORIGIN

Query Match 56.7%; Score 13.6; DB 6; Length 26;
Best Local Similarity 80.0%; Pred. No. 2.8e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 ccaagcagcagcaattctg 22
|||||
Db 3 CCAAGCGCAGGACATTCTG 22

RESULT 7
LOCUS AR087621 26 bp DNA
DEFINITION Sequence 51 from patent US 5989538.
ACCESSION AR087621
VERSION AR087621.1 GI:10014384
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 26)
TITLE Elliot,S.G.
JOURNAL Mpl ligand analogs
FEATURES Patent: US 5989538-A 51 23-NOV-1999;
Location/Qualifiers
source 1..26
BASE COUNT 8 a 7 c 8 g 3 t
ORIGIN

Query Match 56.7%; Score 13.6; DB 6; Length 26;
Best Local Similarity 80.0%; Pred. No. 2.8e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 ccaagcagcagcaattctg 22
|||||
Db 3 CCAAGCGCAGGACATTCTG 22

RESULT 8
LOCUS A06322/c 48 bp DNA
DEFINITION Artificial sequence for HBV antigen.
ACCESSION A06322
VERSION A06322.1 GI:412823
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 48)
AUTHORS Bishop,D.H.L. and Kang,C.Y.
TITLE Expression of hepatitis b viral antigens from recombinant baculovirus vectors

JOURNAL Patent: EP 0260090-A 3 16-MAR-1988;
Bishop, David H.L.; Kang, Chli-Yong
FEATURES Location/Qualifiers
source 1..48
CDS
1..48
/organism="synthetic construct"
/db_xref="taxon:32630"
10..>48
/codon_start=1
/transl_table=11
/product="HBV antigen"
/protein_id="CAA00538.1"
/db_xref="GI:412824"
/translation="MWNSTALHQAIO"
BASE COUNT 11 a 14 c 12 g 11 t
ORIGIN

Query Match 56.7%; Score 13.6; DB 6; Length 48;
Best Local Similarity 80.0%; Pred. No. 2.9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 gtccaagcagcagcaatttc 20
|||||
Db 36 GTCCAAGCGCAGTGGAATTC 17

RESULT 9
LOCUS A06323 48 bp DNA
DEFINITION Artificial sequence for HBV antigen, reverse complement.
ACCESSION A06323
VERSION A06323.1 GI:411244
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 48)
AUTHORS Bishop,D.H.L. and Kang,C.Y.
TITLE Expression of hepatitis b viral antigens from recombinant baculovirus vectors
JOURNAL Patent: EP 0260090-A 4 16-MAR-1988;
Bishop, David H.L.; Kang, Chli-Yong
FEATURES Location/Qualifiers
source 1..48
BASE COUNT 11 a 12 c 14 g 11 t
ORIGIN

Query Match 56.7%; Score 13.6; DB 6; Length 48;
Best Local Similarity 80.0%; Pred. No. 2.9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 gtccaagcagcagcaatttc 20
|||||
Db 17 GTCCAAGCGCAGTGGAATTC 36

RESULT 10
LOCUS AX033196/c 48 bp DNA
DEFINITION Sequence 7 from Patent W00046383.
ACCESSION AX033196
VERSION AX033196.1 GI:10280048
KEYWORDS
SOURCE Madagascar periwinkle.
ORGANISM Catharanthus roseus
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae; Vincaeae; Catharanthus.
1 (bases 1 to 48)

AUTHORS Memelink, J., Kijne, J.W., Menke, F.L. and van der Fits, C.T.
TITLE Method of modulating metabolite biosynthesis in recombinant cells
JOURNAL Patent: WO 0046383-A 7 10-AUG-2000;
UNIV LEIDEN (NL); MEMELINK JOHAN (NL); FITS CORNELIA THEODORA
ELISABE (NL); KIJNE JAN WILLEM (NL); MENKE FRANK LEONARDUS
HENDRIKU (NL)

FEATURES
Source Location/Qualifiers
1..48
/organism="Catharanthus roseus"
/db_xref="taxon:4058"

BASE COUNT 10 a 14 c 8 g 16 t
ORIGIN

Query Match 56.7%; Score 13.6; DB 6; Length 48;
Best Local Similarity 80.0%; Pred. No. 2.9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 gtccaagcagagcaattc 20
Db 47 GTCCAAGCAGAAATCCTTTC 28

RESULT 11
LOCUS A59035 41 bp DNA PAT 06-MAR-1998
DEFINITION Sequence 23 from Patent EP0753581.
ACCESSION A59035
VERSION A59035.1 GI:3714470
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 41)
AUTHORS Schefflinger, F.D., Antoine, G.D., Falkner, Falco-Guenter, D.,
Dorner, F.P. and Eibl, J.D.
TITLE Improved recombinant eukaryotic cytoplasmic viruses, method for
their production and their use as vaccines
JOURNAL Patent: EP 0753581-A 23 15-JAN-1997;
IMMUNO AG (AT)

FEATURES
Source Location/Qualifiers
1..41
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 10 a 11 c 13 g 7 t
ORIGIN

Query Match 55.8%; Score 13.4; DB 6; Length 41;
Best Local Similarity 93.3%; Pred. No. 3.7e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 tccaagcagagcaaa 16
Db 16 TCCAAGCAGAGGCCA 2

RESULT 12
LOCUS A59036 45 bp DNA PAT 06-MAR-1998
DEFINITION Sequence 24 from Patent EP0753581.
ACCESSION A59036
VERSION A59036.1 GI:3714471
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 45)
AUTHORS Schefflinger, F.D., Antoine, G.D., Falkner, Falco-Guenter, D.,
Dorner, F.P. and Eibl, J.D.
TITLE Improved recombinant eukaryotic cytoplasmic viruses, method for
their production and their use as vaccines
JOURNAL Patent: EP 0753581-A 24 15-JAN-1997;

FEATURES IMMUNO AG (AT)
Location/Qualifiers
Source 1..45
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 8 a 14 c 12 g 11 t
ORIGIN

Query Match 55.8%; Score 13.4; DB 6; Length 45;
Best Local Similarity 93.3%; Pred. No. 3.7e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 tccaagcagagcaaa 16
Db 30 TCCAAGCAGAGGCCA 44

RESULT 13
LOCUS AX130478 19 bp DNA PAT 15-MAY-2001
DEFINITION Sequence 1696 from Patent WO0130362.
ACCESSION AX130478
VERSION AX130478.1 GI:14136783
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 19)
AUTHORS Robbins, J.M. and Trletz, R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 1696 03-MAY-2001;
IMMUSOL, INC. (US)

FEATURES
Source Location/Qualifiers
1..19
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Cyclin C ribozyme binding site"

BASE COUNT 8 a 2 c 4 g 5 t
ORIGIN

Query Match 55.0%; Score 13.2; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 4.5e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 tccaagcagagcaattt 19
Db 2 TCCAAGTAGAGCAATTT 19

RESULT 14
LOCUS AX145829 21 bp DNA PAT 31-MAY-2001
DEFINITION Sequence 20 from Patent WO0134840.
ACCESSION AX145829
VERSION AX145829.1 GI:14284347
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 21)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE Genetic compositions and methods
JOURNAL Patent: WO 0134840-A 20 17-MAY-2001;
GLAXO GROUP LIMITED (GB); Affymetrix, Inc. (US)

FEATURES
Source Location/Qualifiers
1..21
/organism="Homo sapiens"
/db_xref="taxon:9606"

variation 1..21
 /note="v' represents a polymorphic base"
 BASE COUNT 6 a 4 c 4 g 6 t 1 others
 ORIGIN

Query Match 55.0%; Score 13.2; DB 6; Length 21;
 Best Local Similarity 78.9%; Pred. No. 4.5e+04;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 agcgagagcaattctgca 24
 || ||||| ||||| ||
 Db 20 ATGAAGAGCNAATTCTCTCA 2

RESULT 15

AX111191 23 bp DNA PAT 30-APR-2001
 LOCUS
 DEFINITION Sequence 1924 from Patent WO0123604.
 ACCESSION AX111191
 VERSION AX111191.1 GI:13927483

KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 artificial sequence.

REFERENCE 1 (bases 1 to 23)
 AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
 Picard,F.J. and Roy,P.H.

TITLE Highly conserved genes and their use to generate probes and primers
 JOURNAL for detection of microorganisms

Patent: WO 0123604-A 1924 05-APR-2001;
 Infectio Diagnostic (I.D.I.) INC. (CA)

FEATURES
 Source Location/Qualifiers

1..23
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Oligonucleotide"
 BASE COUNT 4 a 5 c 4 g 10 t
 ORIGIN

Query Match 55.0%; Score 13.2; DB 6; Length 23;
 Best Local Similarity 83.3%; Pred. No. 4.5e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 tcgaagcgagcaattt 19
 ||||| || ||||| ||
 Db 5 TCCAATGCTGAGCACTTT 22

Search completed: March 9, 2002, 00:48:44
 Job time: 11125 sec

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